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10/533277

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SEQUENCE LISTING

<110> National Institute of Agrobiological Sciences

<120> METHODS FOR DETERMINING GENETIC RESISTANCE OF PIGS TO DISEASES CAUSED
BY RNA VIRUSES

<130> MOA-A0214P

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<150> JP 2002-313076

<151> 2002-10-28

<160> 10

<170> PatentIn Ver. 2.1

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<211> 2545

<212> DNA

<213> Sus scrofa

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<221> CDS

<222> (101)..(2092)

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<221> polyA_signal

<222> (2517)..(2522)

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Met Val Tyr Ser Ser

1 5

tgt gaa agt aaa gaa cct gat tca gtt tct gca tcc aat cac ctg tta 163

Cys Glu Ser Lys Glu Pro Asp Ser Val Ser Ala Ser Asn His Leu Leu

10 15 20

cta aat ggg aat gat gaa ttg gtg gag aaa agt cac aaa aca ggg cct 211

Leu Asn Gly Asn Asp Glu Leu Val Glu Lys Ser His Lys Thr Gly Pro

25 30 35

gag aac aac ctg tac agc cag tac gag gag aaa gtg cgg ccc tgc atc 259

Glu Asn Asn Leu Tyr Ser Gln Tyr Glu Glu Lys Val Arg Pro Cys Ile

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gac ctc atc gac tca ctg cgg gcc ctg ggc gtg gag cag gac ctg gcc 307

Asp Leu Ile Asp Ser Leu Arg Ala Leu Gly Val Glu Gln Asp Leu Ala

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ctg ccc gcc atc gcc gtc atc ggg gac cag agt tcg ggc aag agc tcc 355

Leu Pro Ala Ile Ala Val Ile Gly Asp Gln Ser Ser Gly Lys Ser Ser

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gtg ctg gag gcc ctg tcg ggg gtc gct ctc ccc aga ggc agc gga att 403

Val Leu Glu Ala Leu Ser Gly Val Ala Leu Pro Arg Gly Ser Gly Ile

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gtg aca aga tgc cct ctt gtg ctg aaa ttg aaa aaa ctc gtg aac gaa 451

Val Thr Arg Cys Pro Leu Val Leu Lys Leu Lys Lys Leu Val Asn Glu

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gaa gac gaa tgg aag ggc aaa gtc agt tac cgg gac agc gag att gag 499

Glu Asp Glu Trp Lys Gly Lys Val Ser Tyr Arg Asp Ser Glu Ile Glu

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ctt tca gat gct tcg cag gtg gaa aag gaa gtc agc gca gcc cag att 547

Leu Ser Asp Ala Ser Gln Val Glu Lys Glu Val Ser Ala Ala Gln Ile

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gcc atc gct ggg gaa ggc gtg gga atc agt cat gag cta atc agt ctg 595

Ala Ile Ala Gly Glu Gly Val Gly Ile Ser His Glu Leu Ile Ser Leu

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gag gtc agc tcc cct cat gtc cca gat ctg acc ctc ata gac ctt cct 643
 Glu Val Ser Ser Pro His Val Pro Asp Leu Thr Leu Ile Asp Leu Pro
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ggc atc acc agg gta gct gta ggc aat cag cca tac gac atc gaa tac 691
 Gly Ile Thr Arg Val Ala Val Gly Asn Gln Pro Tyr Asp Ile Glu Tyr
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cag atc aag tct ctg atc aag aag tac atc tgt aag cag gag acc atc 739
 Gln Ile Lys Ser Leu Ile Lys Tyr Ile Cys Lys Gln Glu Thr Ile
 200 205 210

aac ttg gtg gtg gtc ccc tgt aac gtg gac att gcc acc acg gag gcg 787
 Asn Leu Val Val Pro Cys Asn Val Asp Ile Ala Thr Thr Glu Ala
 215 220 225

ctg cgc atg gcc cag gag gtg gac ccc gaa gga gac agg acc atc ggg 835
 Leu Arg Met Ala Gln Glu Val Asp Pro Glu Gly Asp Arg Thr Ile Gly
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atc ttg acg aag ccg gat ctg gtg gac aaa ggc act gag gac aag ata 883
 Ile Leu Thr Lys Pro Asp Leu Val Asp Lys Gly Thr Glu Asp Lys Ile
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gtg gac gtg gcg aga aac ctg gtc ttc cac ctg aag aag ggc tac atg 931

Val Asp Val Ala Arg Asn Leu Val Phe His Leu Lys Lys Gly Tyr Met
 265 270 275

att gtc aag tgc agg ggc cag cag gac atc cag gag cag ctg agc ctg 979
 Ile Val Lys Cys Arg Gly Gln Gln Asp Ile Gln Glu Gln Leu Ser Leu
 280 285 290

gcc aag gcc ctg cag aag gag cag gcc ttc ttt gaa aac aac cac gca cat 1027
 Ala Lys Ala Leu Gln Lys Glu Gln Ala Phe Phe Glu Asn His Ala His
 295 300 305

ttc agg gat ctt ctg gag gaa ggg cgg gcc acg atc ccc tgc ctg gca 1075
 Phe Arg Asp Leu Leu Glu Glu Gly Arg Ala Thr Ile Pro Cys Leu Ala
 310 315 320 325

gaa aga ctg acc tct gaa ctc atc atg cac atc tgt aaa act ctg ccc 1123
 Glu Arg Leu Thr Ser Glu Leu Ile Met His Ile Cys Lys Thr Leu Pro
 330 335 340

ctg tta gaa aac caa ata aaa gag agt cac cac aaa ata aca gag gag 1171
 Leu Leu Glu Asn Gln Ile Lys Glu Ser His Gln Lys Ile Thr Glu Glu
 345 350 355

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 Leu Gln Lys Tyr Gly Ser Asp Ile Pro Glu Asp Glu Ser Gly Lys Met
 360 365 370

ttt ttt ctg ata gat aaa atc gat gca ttt aat agt gat atc act gct	1267	
Phe Phe Leu Ile Asp Lys Ile Asp Ala Phe Asn Ser Asp Ile Thr Ala		
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ttg ata caa gga gag gaa ctg gtg gtg gag tac gag tgt cgg ctg ttt	1315	
Leu Ile Gln Gly Glu Glu Leu Val Val Glu Tyr Glu Cys Arg Leu Phe		
390	395	400
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acc aag atg cga aat gag ttc tgc aga tgg agt gct gtg gtt gaa aag	1363	
Thr Lys Met Arg Asn Glu Phe Cys Arg Trp Ser Ala Val Val Glu Lys		
410	415	420
aat ttc aaa aat ggt tat gac gcc ata tgt aaa caa atc cag ctc ttc	1411	
Asn Phe Lys Asn Gly Tyr Asp Ala Ile Cys Lys Gln Ile Gln Leu Phe		
425	430	435
gaa aat cag tac agg ggg aga gag ttg cca ggg ttt gtg aat tat aag	1459	
Glu Asn Gln Tyr Arg Gly Arg Glu Leu Pro Gly Phe Val Asn Tyr Lys		
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aca ttt gaa acc atc att aag aag cag gtc agt gtc ctg gaa gag cca	1507	
Thr Phe Glu Thr Ile Ile Lys Lys Gln Val Ser Val Leu Glu Glu Pro		
455	460	465
gcc gtg gac atg ctg cac aca gtg act gat tta gtc cgg ctc gcc ttc	1555	

Ala Val Asp Met Leu His Thr Val Thr Asp Leu Val Arg Leu Ala Phe
 470 475 480 485

aca gat gtt tca gaa aca aat ttt aat gaa ttt ttc aac ctc cac aga 1603
 Thr Asp Val Ser Glu Thr Asn Phe Asn Glu Phe Phe Asn Leu His Arg
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act gcc aag tcc aaa att gaa gac att aaa tta gaa caa gaa aaa gaa 1651
 Thr Ala Lys Ser Lys Ile Glu Asp Ile Lys Leu Glu Gln Glu Lys Glu
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gct gag acg tcg atc cgg ctc cac ttc caa atg gag cag atc gtg tac 1699
 Ala Glu Thr Ser Ile Arg Leu His Phe Gln Met Glu Gln Ile Val Tyr
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tgc cag gac cag gtc tat cgg ggc gcg ctg cag aag gtc aga gag aag 1747
 Cys Gln Asp Gln Val Tyr Arg Gly Ala Leu Gln Lys Val Arg Glu Lys
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 Glu Ala Glu Glu Glu Lys Asn Arg Lys Ser Asn Gln Tyr Phe Leu Ser
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 Ser Pro Ala Pro Ser Ser Asp Pro Ser Ile Ala Glu Ile Phe Gln His
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Leu Ile Ala Tyr His Gln Glu Val Gly Lys Arg Ile Ser Ser His Ile

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cct ctg atc atc cag ttc ttc atc ctc cgg acc ttt ggg cag cag ctg 1939

Pro Leu Ile Ile Gln Phe Phe Ile Leu Arg Thr Phe Gly Gln Gln Leu

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cag aag agc atg ctg cag ctg cag aac aag gac caa tac gac tgg 1987

Gln Lys Ser Met Leu Gln Leu Leu Gln Asn Lys Asp Gln Tyr Asp Trp

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ctc ctg agg gag cgc agt gac acc agc gac aag agg aag ttc ctg aag 2035

Leu Leu Arg Glu Arg Ser Asp Thr Ser Asp Lys Arg Lys Phe Leu Lys

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gag cgg ctg atg cgg ctg acc cag gct cgg cgc cgg ctc gcc aag ttc 2083

Glu Arg Leu Met Arg Leu Thr Gln Ala Arg Arg Arg Leu Ala Lys Phe

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cca ggc tga accggactct ccaggcggcc cggggctctcc agggcacgtc 2132

Pro Gly

tccaggcaac gaggaccaac ctcctccct aacagactag catcatgagc tcctgttcg 2192

cacatcctcc tgtggtagt agactctaaa gccaccgtcc ctgctgttag tggctgagga 2252

cttagcaaga agctgtgata agcacgctgg ctgcaagcat caggccattt acttgaatga 2312

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tccctgtata ggatactggt ccccgcatag catcatagaa gggtcattct ggtttctgta 2432

caagccttc acgccaatg tcttagggc attacagcca cctgtgtgga tggatgcaca 2492

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His Lys Thr Gly Pro Glu Asn Asn Leu Tyr Ser Gln Tyr Glu Glu Lys

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Val Arg Pro Cys Ile Asp Leu Ile Asp Ser Leu Arg Ala Leu Gly Val

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Glu Gln Asp Leu Ala Leu Pro Ala Ile Ala Val Ile Gly Asp Gln Ser

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Ser Gly Lys Ser Ser Val Leu Glu Ala Leu Ser Gly Val Ala Leu Pro

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Arg Gly Ser Gly Ile Val Thr Arg Cys Pro Leu Val Leu Lys Leu Lys

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Lys Leu Val Asn Glu Glu Asp Glu Trp Lys Gly Lys Val Ser Tyr Arg

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120

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Asp Ser Glu Ile Glu Leu Ser Asp Ala Ser Gln Val Glu Lys Glu Val

130

135

140

Ser Ala Ala Gln Ile Ala Ile Ala Gly Glu Gly Val Gly Ile Ser His

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Glu Leu Ile Ser Leu Glu Val Ser Ser Pro His Val Pro Asp Leu Thr

165

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175

Leu Ile Asp Leu Pro Gly Ile Thr Arg Val Ala Val Gly Asn Gln Pro
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Tyr Asp Ile Glu Tyr Gln Ile Lys Ser Leu Ile Lys Lys Tyr Ile Cys
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Lys Gln Glu Thr Ile Asn Leu Val Val Val Pro Cys Asn Val Asp Ile
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Ala Thr Thr Glu Ala Leu Arg Met Ala Gln Glu Val Asp Pro Glu Gly
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Asp Arg Thr Ile Gly Ile Leu Thr Lys Pro Asp Leu Val Asp Lys Gly
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Thr Glu Asp Lys Ile Val Asp Val Ala Arg Asn Leu Val Phe His Leu
260 265 270

Lys Lys Gly Tyr Met Ile Val Lys Cys Arg Gly Gln Gln Asp Ile Gln
275 280 285

Glu Gln Leu Ser Leu Ala Lys Ala Leu Gln Lys Glu Gln Ala Phe Phe
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Glu Asn His Ala His Phe Arg Asp Leu Leu Glu Glu Gly Arg Ala Thr
305 310 315 320

Ile Pro Cys Leu Ala Glu Arg Leu Thr Ser Glu Leu Ile Met His Ile

325

330

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Cys Lys Thr Leu Pro Leu Leu Glu Asn Gln Ile Lys Glu Ser His Gln

340

345

350

Lys Ile Thr Glu Glu Leu Gln Lys Tyr Gly Ser Asp Ile Pro Glu Asp

355

360

365

Glu Ser Gly Lys Met Phe Phe Leu Ile Asp Lys Ile Asp Ala Phe Asn

370

375

380

Ser Asp Ile Thr Ala Leu Ile Gln Gly Glu Glu Leu Val Val Glu Tyr

385

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395

400

Glu Cys Arg Leu Phe Thr Lys Met Arg Asn Glu Phe Cys Arg Trp Ser

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Ala Val Val Glu Lys Asn Phe Lys Asn Gly Tyr Asp Ala Ile Cys Lys

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Gln Ile Gln Leu Phe Glu Asn Gln Tyr Arg Gly Arg Glu Leu Pro Gly

435

440

445

Phe Val Asn Tyr Lys Thr Phe Glu Thr Ile Ile Lys Lys Gln Val Ser

450

455

460

Val Leu Glu Glu Pro Ala Val Asp Met Leu His Thr Val Thr Asp Leu

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475

480

Val Arg Leu Ala Phe Thr Asp Val Ser Glu Thr Asn Phe Asn Glu Phe

485

490

495

Phe Asn Leu His Arg Thr Ala Lys Ser Lys Ile Glu Asp Ile Lys Leu

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505

510

Glu Gln Glu Lys Glu Ala Glu Thr Ser Ile Arg Leu His Phe Gln Met

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520

525

Glu Gln Ile Val Tyr Cys Gln Asp Gln Val Tyr Arg Gly Ala Leu Gln

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535

540

Lys Val Arg Glu Lys Glu Ala Glu Glu Lys Asn Arg Lys Ser Asn

545

550

555

560

Gln Tyr Phe Leu Ser Ser Pro Ala Pro Ser Ser Asp Pro Ser Ile Ala

565

570

575

Glu Ile Phe Gln His Leu Ile Ala Tyr His Gln Glu Val Gly Lys Arg

580

585

590

1 4 / 1 8

Ile Ser Ser His Ile Pro Leu Ile Ile Gln Phe Phe Ile Leu Arg Thr

595

600

605

Phe Gly Gln Gln Leu Gln Lys Ser Met Leu Gln Leu Leu Gln Asn Lys

610

615

620

Asp Gln Tyr Asp Trp Leu Leu Arg Glu Arg Ser Asp Thr Ser Asp Lys

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Arg Lys Phe Leu Lys Glu Arg Leu Met Arg Leu Thr Gln Ala Arg Arg

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Arg Leu Ala Lys Phe Pro Gly

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